

Gencore version 5.1.3
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On protein - protein search, using sw model.

Run on: December 19, 2002, 14:56:27 ; Search time 14 Seconds
(without alignments)
1679.791 Million cell updates/sec

Title: US-08-813-323B-1

Perfect score: 2994

Sequence: 1 MESSKKDAAGILQPNPLK.....1KDDTIFIKVIVDSDLRDP 567

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40;*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2994	100.0	567	1 TRA3_MOUSE
2	2885	96.4	568	1 TRA3_HUMAN
3	837.5	28.0	501	1 TRA2_MOUSE
4	745.5	24.9	501	1 TRA2_HUMAN
5	641.5	21.4	416	1 TRA1_MOUSE
6	640	21.4	409	1 TRA1_MOUSE
7	209	7.0	458	1 DGT1_DICCI
8	168	5.6	1816	1 LMA1_MOUSE
9	164	5.5	919	1 RA50_AERPE
10	161	5.4	634	1 2147_MOUSE
11	157.5	5.3	1102	1 MYSC_CHICK
12	151.5	5.1	704	1 MEBP_MOUSE
13	149	5.0	1957	1 YB61_SCHOO
14	147	4.9	1816	1 LMA1_HUMAN
15	147	4.9	2230	1 GOG4_HUMAN
16	147	4.9	3210	1 CENF_HUMAN
17	146	4.9	1679	1 Y100_YEAST
18	146	4.9	1727	1 AML1_SCHOO
19	145.5	4.9	944	1 NUFL1 YEAST
20	145	4.8	624	1 A33_PLEWA
21	145	4.8	1005	1 RA50_METRA
22	144.5	4.8	1 TM31_HUMAN	homo sapien
23	144	4.8	1935	1 MIH7_RAT
24	142.5	4.8	794	1 HMMR_MOUSE
25	142.5	4.8	1940	1 MYH3_RAT
26	141.5	4.7	1935	1 MYH3_HUMAN
27	141	4.7	1940	1 MYH3_CHICK
28	140.5	4.7	886	1 RA50_ARCFC
29	140.5	4.7	1934	1 MYH7_MESAU
30	140	4.7	879	1 RA50_PYRHO
31	139.5	4.7	1940	1 MYH3_HUMAN
32	139	4.6	1790	1 USO1 YEAST
33	139	4.6	1938	1 MYHD_HUMAN

ALIGNMENTS

RESULT 1

TRAF3_MOUSE	ID	TRA3_MOUSE	STANDARD;	PRT:	567 AA.
SEQUENCE FROM N.A.	AC	060803	MUS MUSCULUS	DT	30-MAY-2000 (Rel. 39, Created)
STRAIN=C57BL/6J; TISSUE=Brain;	DT	060803	Q13114	DT	30-MAY-2000 (Rel. 39, Last sequence update)
MEDLINE=95184010; PubMed=7533327;	RA	019233	homo sapien	DT	15-JUN-2002 (Rel. 41, Last annotation update)
Cheng G., Cleary A.M., Ye Z., Hong D.I., Lederman S., Baltimore D.;	RA	013077	homo sapien	DE	TNF receptor associated factor 3 (CD40 receptor associated factor 1)
"Involvement of Craf1, a relative of TRAF, in CD40 signaling.";	RA	0139428	mus musculus	DE	(CRAF1) (TRAFM).
Dinulos M.B., Disteche C.M., Copeland N.G., Gilbert D.J., Jenkins N.A., Lacy E., Wang X., Bornslaeger E.A., Haub O., Tomihara-Newberger C., Lonberg N.,	RA	0139429	mus musculus	DE	TRA3 OR CRAFT OR TRAFAN.
"A candidate gene for the amionless gastrulation stage mouse mutation encodes a TRAF-related protein.";	RA	0139430	mus musculus	OS	Mus musculus (Mouse).
Dev. Biol. 177:274-290(1996).	RL	0139431	drosophila	OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
Science 267:1494-1498(1995).	RL	0139432	mus musculus	OX	NCBI_TAXID=10090;
[2]	RN	0139433	rat	RN	[1]
SEQUENCE FROM N.A.	RN	0139434	rat	RN	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=95184010; PubMed=7533327;	RX	0139435	rat	RX	SEQUENCE FROM N.A.
Cheng G., Cleary A.M., Ye Z., Hong D.I., Lederman S., Baltimore D.;	RX	0139436	rat	RX	STRAIN=C57BL/6J; TISSUE=Brain;
"Involvement of Craf1, a relative of TRAF, in CD40 signaling.";	RX	0139437	rat	RX	MEDLINE=95184010; PubMed=7533327;
Dinulos M.B., Disteche C.M., Copeland N.G., Gilbert D.J., Jenkins N.A., Lacy E., Wang X., Bornslaeger E.A., Haub O., Tomihara-Newberger C., Lonberg N.,	RA	0139438	rat	RA	Cheng G., Cleary A.M., Ye Z., Hong D.I., Lederman S., Baltimore D.;
"A candidate gene for the amionless gastrulation stage mouse mutation encodes a TRAF-related protein.";	RA	0139439	rat	RA	"Involvement of Craf1, a relative of TRAF, in CD40 signaling.";
Dev. Biol. 177:274-290(1996).	RL	0139440	rat	RL	Science 267:1494-1498(1995).
- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 kDa TUMOR NECROSIS FACTOR RECEPTOR (TNFR-R2). ALSO BINDS TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR (BY SIMILARITY).	CC	0139441	rat	CC	[2]
- SUBUNIT: HOMODIMER OR HETERO DIMER WITH OTHER TNF RECEPTOR ASSOCIATED FACTORS (POTENTIAL).	CC	0139442	rat	CC	- SUBUNIT: HOMODIMER OR HETERO DIMER WITH OTHER TNF RECEPTOR ASSOCIATED FACTORS (POTENTIAL).
- TISSUE SPECIFICITY: IN ADULT, HIGHEST IN BRAIN. ALSO FOUND IN KIDNEY, HEART, THYMUS, SPLEEN, LUNG, MUSCLE, TESTIS AND OVARY. NOT FOUND IN LIVER.	CC	0139443	rat	CC	- TISSUE SPECIFICITY: IN ADULT, HIGHEST IN BRAIN. ALSO FOUND IN KIDNEY, HEART, THYMUS, SPLEEN, LUNG, MUSCLE, TESTIS AND OVARY. NOT FOUND IN LIVER.
- DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED FROM 6.5. HIGHEST LEVELS FOUND BETWEEN E11.5 AND E13.5. AT LATE STAGES OF GESTATION, FROM E14.5, ONLY LOW LEVELS ARE DETECTED.	CC	0139444	rat	CC	- DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED FROM 6.5. HIGHEST LEVELS FOUND BETWEEN E11.5 AND E13.5. AT LATE STAGES OF GESTATION, FROM E14.5, ONLY LOW LEVELS ARE DETECTED.
- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	CC	0139445	rat	CC	- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
- SIMILARITY: CONTAINS 2 TRAF-TYPE LINC FINGERS.	CC	0139446	rat	CC	- SIMILARITY: CONTAINS 2 TRAF-TYPE LINC FINGERS.
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EMBL; MGI; U21050; AAC52175.1; -	DR	0139448	rat	DR	EMBL; MGI; U21050; AAC52175.1; -
MGI; U33840; AAC52175.1; -	DR	0139449	rat	DR	MGI; U33840; AAC52175.1; -
MGI; U08041; Traf3.	DR	0139450	rat	DR	MGI; U08041; Traf3.

DR InterPro; IPR002083; MATH.
 DR InterPro; IPR03007; TRAF.
 DR InterPro; IPR01193; Znf_TRAF.
 DR Pfam; PF00097; zf-C3H4; 1.
 DR Pfam; PF02176; zf-TRAF; 2.
 DR SMART; SM0061; MATH; 1.
 DR PROSITE; PS00518; ZF_RING_1; 1.
 DR PROSITE; PS0089; ZF_RING_2; 1.
 DR PROSITE; PS0145; ZF_TRAF; 2.
 KW Zinc-finger; Coiled coil; Repeat.
 FT ZN_FING 67 76 RING-TYPE.
 FT ZN_FING 134 189 TRAF-TYPE 1.
 FT DOMAIN 190 248 TRAF-TYPE 2.
 FT DOMAIN 266 337 COILED COIL (POTENTIAL).
 FT DOMAIN 417 502 MATH/TRAF.
 FT CONFLICT 72 73 CE -> WQ (IN REF. 2).
 FT CONFLICT 390 390 T -> M (IN REF. 2).
 SQ SEQUENCE 567 AA: 64263 MW: 2522B343B41192DC CRC64:
 Query Match 100.0%; Score 2994; DB 1; Length 567;
 Best Local Similarity 100.0%; Pred. No. 1; e-value: 1.72;
 Matches 567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MESSKKMDAAGTLQPNPPLKLQPDROGSVLPWPEOGGYKPFVKFVTDYKCKCERLVLIC 60
 DB 1 MESSKKMDAAGTLQPNPPLKLQPDROGSVLPWPEOGGYKPFVKFVTDYKCKCERLVLIC 60
 QY 61 NPKOTRSGHRGCECSCHALSSSSPKCTACOESIHKVKPFKDNCRELLALQYCRNEG 120
 DB 61 NPKOTRSGHRGCECSCHALSSSSPKCTACOESIHKVKPFKDNCRELLALQYCRNEG 120
 QY 121 RGCABDQLTGHILLVHLKNEQFFELPCLRADCKEVRKLRLDRDHLVEACKYRATCOSH 180
 DB 121 RGCABDQLTGHILLVHLKNEQFFELPCLRADCKEVRKLRLDRDHLVEACKYRATCOSH 180
 QY 181 SQVPMKILQKEDTPCPVVWSCPHCSVTLRSELSEHLSCVNAPSTCISRRYGCVF 240
 DB 181 SQVPMKILQKEDTPCPVVWSCPHCSVTLRSELSEHLSCVNAPSTCISRRYGCVF 240
 QY 241 QGTNQOKIAHEASSAVQHVHLKNSLEKKVSLQNSVEKNSQIOLHNQCSFE 300
 DB 241 QGTNQOKIAHEASSAVQHVHLKNSLEKKVSLQNSVEKNSQIOLHNQCSFE 300
 QY 301 TERQKEMLRNNESKTLHLQRVIDSQAEKIKELDEKEIRPRERNNPREADMSKSSESLQRV 360
 DB 301 TERQEMLRNNESKTLHLQRVIDSQAEKIKELDEKEIRPRERNNPREADMSKSSESLQRV 360
 QY 361 TELESVDKSAGQAARNTGLESQLSRHDTLSVDIRADMDFRQVETASVNGVLWK 420
 DB 361 TELESVDKSAGQAARNTGLESQLSRHDTLSVDIRADMDFRQVETASVNGVLWK 420
 QY 421 IRDKKRKQDAVMGKTLYSQPPYTGFGYKACARVINGDGKGTHLSLFVTRGE 480
 DB 421 IRDKKRKQDAVMGKTLYSQPPYTGFGYKACARVINGDGKGTHLSLFVTRGE 480
 QY 481 YDALLPWPFKQVTLMLMQGSSRHLQDFAKDPNSSFKRPGETGEMTIASGCCPVFAQT 540
 DB 481 YDALLPWPFKQVTLMLMQGSSRHLQDFAKDPNSSFKRPGETGEMTIASGCCPVFAQT 540
 QY 541 VLENQTYIKDTTPIKVIVTSQDLPDP 567
 DB 541 VLENQTYIKDTTPIKVIVTSQDLPDP 567
 RESULT 2
 TRA3_HUMAN STANDARD PRT: 568 AA.
 ID TRA3_HUMAN STANDARD PRT: 568 AA.
 AC Q13114; Q13076; Q13947; Q12990;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DR MEDLINE-9516392; PubMed=7859281;
 DR MEDLINE-9516392; PubMed=753327;
 DR Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
 DR "Involvement of Craf1, a relative of TRAF, in CD40 signaling.";
 DR Science 267:1494-1498(1995).
 DR [2]
 DR SEQUENCE FROM N.A., AND CHARACTERIZATION.
 DR TISSUE-Lymphoma;
 DR MEDLINE-9516392; PubMed=753327;
 DR Mosalios G., Birkenbach M., Yalamanchili R., Vanarsdale T., Ware C.,
 DR Kieff E.;
 DR "The Epstein-Barr virus transforming protein LMP1 engages signaling
 proteins for the tumor necrosis factor receptor family.";
 DR Cell 80:389-399(1995).
 DR [3]
 DR SEQUENCE FROM N.A.
 DR TISSUE=Petal brain;
 DR MEDLINE-95129692; PubMed=7530216;
 DR Sato T., Irie S., Reed J.C.;
 DR "A novel member of the TRAF family of putative signal transducing
 proteins binds to the cytosolic domain of CD40.";
 DR RT FEBS Lett. 358:113-118(1995).
 DR SEQUENCE FROM N.A.
 DR MEDLINE-95073988; PubMed=7527023;
 DR Hu H.M., O'Rourke K., Boguski M.S., Dixit V.M.;
 DR "A novel RING finger protein interacts with the cytoplasmic domain of
 CD40.";
 DR J. Biol. Chem. 269:30069-30072(1994).
 DR CC OF THE 75 kDa TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
 DR TO CD40 AND THE LYMPHOTOXIN- β RECEPTOR
 DR - - SUBUNIT: HOMODIMER OR HETEROODIMER WITH OTHER TNF RECEPTOR
 DR ASSOCIATED FACTORS (POENTIAL).
 DR CC - - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR CC - - FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
 DR CC - - SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.
 DR CC - - SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
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 DR CC or send an email to license@isb-sib.ch).
 DR CC -----
 DR EMBL; U21092; AAC50112.1; -;
 DR EMBL; U19260; AAA65732.1; -;
 DR EMBL; L38509; AAA68195.1; -;
 DR EMBL; U15637; AAA56753.1; -;
 DR Genew; HGNC-12033; TRAF3.
 DR MM; 601896; -;
 DR InterPro; IPR002083; MATH.
 DR InterPro; IPR03007; TRAF.
 DR InterPro; IPR01293; Znf_RING.
 DR InterPro; IPR01841; Znf_RING.
 DR Pfam; PF00097; zf-C3H4; 1.
 DR Pfam; PF00917; MATH; 1.
 DR InterPro; IPR03007; TRAF.
 DR InterPro; IPR01293; Znf_TRAF.
 DR SMART; SM0061; MATH; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00518; ZF_RING_1; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.

DR PROSITE: PS50145; ZF TRAF; 2.
 KW Zinc-finger; Coiled coil; Repeat.
 FT ZN_FING 68 77 RING-TYPE.
 FT ZN_FING 135 190 TRAF-TYPE 1.
 FT ZN_FING 191 249 TRAF-TYPE 2.
 FT DOMAIN 267 338 COILED COIL (POTENTIAL).
 FT DOMAIN 418 503 MAT/TRAFF.
 FT CONFLICT 129 129 T -> M (IN REF. 2 AND 4).
 FT CONFLICT 134 134 MISSING (IN REF. 4).
 FT CONFLICT 218 242 MISSING (IN REF. 3).
 FT CONFLICT 339 339 P -> S (IN REF. 3).
 FT CONFLICT 405 405 R -> G (IN REF. 4).
 SQ SEQUENCE 568 AA: 64460 MW: 6765533FBF523C8B CRC64;
 Query Match 96.4%; Score 2866.5; DB 1; Length 568;
 Best Local Similarity 96.1%; Pred. No. 3.7-16; Indels 14; Gaps 1; Matches 546; Conservative 7; Mismatches 14; Delins 1; Cuts 1; Gaps 1;
 Oy 1 MESSKKMDAAGTLQPNNPLKQPDGRGS-VVPEQPGYKEKFKVTFEDYKCEKGRFLVL 59
 |||||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
 Db 1 MESSKKMDPSPGALQTNPPLKLTDARSAGTPVFEQGYKEKFKVTFEDYKCEKCHLV 60
 Oy 60 CNPKOTEGGHRFCESCMALLSSSPKCACQSIKQVKVFNDCCRELLALQYCRNE 119
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 61 CSPKQTECGHRFCESCMALLSSSPKCACQSIKQVKVFNDCCRELLALQYCRNE 120
 120 GRGCAGAQLTGHLLVHLKNCFEELPCLRADCKEKFVLDHVACKYREACTCSHC 179
 Oy 121 SRGCAGDQLTGHLLVHLKNCFEELPCLRADCKEKFVLDHVACKYREACTCSHC 180
 Oy 180 KSQVPMKLOKHEDTCPVCVVSCHPKCSVQTLRSLSAHLSBCVNAPSTGSKRYGV 239
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 181 KSQVPMIALQKHEDTCPVCVVSCHPKCSVQTLRSLSAHLSBCVNAPSTGSKRYGV 240
 Oy 240 FGTTNGQIKAHASSAVOHYNLKKWSNSLEKYSVLLQESVEVNKSISQSLHQICSEI 299
 |||||||:|||||:|||||:|||||:|||||:|||||:
 Db 241 FGTTNGQIKAHASSAVOHYNLKKWSNSLEKYSVLLQESVEVNKSISQSLHQICSEI 300
 Oy 300 EERQKEMLRNNEKSKLHLQRVIDSQAEKIKELDKIRPRQNEEAMSKSSVESLQRN 359
 |||||||:|||||:|||||:|||||:|||||:|||||:
 Db 301 ETEROKEMLRNNEKSKLHLQRVIDSQAEKIKELDKIRPRQNEEAMSKSSVESLQRN 360
 Oy 360 VTELESVDKSAGQQAARTGILSLEQLSQRHDQTLVSDIRLADMDFQVLETASYNGVILW 419
 |||||||:|||||:|||||:|||||:|||||:
 Db 361 VTELESVDKSAGQQAARTGILSLEQLSQRHDQTLVSDIRLADMDFQVLETASYNGVILW 420
 Oy 420 KIRDYKRKRQEAQMGKTLSSQPFVYFGYKMCARVYLNGDGNGKGLHSLEFFVIMRG 479
 |||||||:|||||:|||||:|||||:
 Db 421 KIRDYKRKRQEAQMGKTLSSQPFVYFGYKMCARVYLNGDGNGKGLHSLEFFVIMRG 480
 Oy 480 EXDALLPPFKQVTLMLDDGSSRRLGDAFKPDNNSSPKPTEGMNTASGPVFAQ 539
 |||||||:|||||:|||||:|||||:
 Db 481 EXDALLPPFKQVTLMLDDGSSRRLGDAFKPDNNSSPKPTEGMNTASGPVFAQ 540
 Oy 540 TULENGTHIKDMDIFIVIVDSDLPP 567
 |||||||:|||||:
 Db 541 TYLENGLTYIKDDIFIVIVDSDLPP 568
 RESULT 3
 TRA2_MOUSE STANDARD: PRT; 501 AA.
 ID TRA2_MOUSE
 AC P39429;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE TNF receptor associated factor 2 (TRAF2).
 GN TRAF2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=9439371; PubMed=8069916;
 RA Roth M., Wong S.C., Henzel W.J.; Geddel D.V.;
 "A novel family of putative signal transducers associated with the
 cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
 RT Cell 78:681-692(1994).
 RL FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
 OF THE 75 kDa TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND
 ACTIVATES NF-KAPPA-B.
 CC -!- SUBUNIT: HOMODIMER OR HETERO DIMER OF TRAF1 AND TRAF2. THIS
 HETERO COMPLEX CAN BIND TO THE N- TERMINAL OF INHIBITOR OF APOPTOSIS
 PROTEINS 1 AND 2 (IAPS), TO RECRUIT THEM TO THE TUMOR NECROSIS
 FACTOR RECEPTOR 2 (TNFR2).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -!- SIMILARITY: CONTAINS 1 MATH-TYPE ZINC FINGER DOMAIN.
 CC -!- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
 DR EMBL: L33303; AAC37662.1; -.
 DR HSSP: P12351; HWT; Traf2.
 DR MGDB: MGI:10185; Traf2.
 DR InterPro: IPR003007; TRAF.
 DR InterPro: IPR001293; zf-TRAF.
 DR InterPro: IPR001841; Znf-TRAF.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00917; MATH; 1.
 DR Pfam: PF02176; zf-TRAF; 2.
 DR SMART: SM00061; MATH; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00538; ZF_RING-1; 1.
 DR PROSITE: PS50009; ZF_RING-2; 1.
 DR PROSITE: PS50145; ZF_TRAF; 2.
 DR Zinc-finger: Coiled coil; Repeat.
 FT ZN_FING 34 73 RING-TYPE.
 FT ZN_FING 124 180 TRAF-TYPE 1.
 FT ZN_FING 177 233 TRAF-TYPE 2.
 FT DOMAIN 298 348 COILED COIL (POTENTIAL).
 FT DOMAIN 334 501 MATH-TYPE TRAF.
 SQ SEQUENCE 501 AA: 56025 MW: 043391180365FF10 CRC64;
 Query Match 28.0%; Score 837.5; DB 1; Length 501;
 Best Local Similarity 33.5%; Pred. No. 2.3e-43; Indels 99; Gaps 16;
 Matches 194; Conservative 88; Mismatches 198; Delins 1; Cuts 1; Gaps 1;
 Oy 7 MDAAGTLQPNPLKQPDGRGSVLUPEQPGYKEKFKVTFEDYKCEKGRFLVLCNPQQT 65
 |||||:|||:|||:
 Db 1 MAASAVTSPGSLELLQQ-----GFSKILGLTRLEAKYLCSACKNLRRPQA 47
 Oy 66 ECCHRFCESCMALLSSSPKCACQSIKQVKVFNDCCRELLALQYCRNE 116
 |||||:|||:
 Db 48 QCGHRYCSFCFLNSILSSGPONCAACVYEGIYEEGISILESSAAPPDNAAARRREVESLPAVC 107
 Oy 117 RNEGRGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKFVLDHVACKYREACTC 176
 |||||:|||:
 Db 108 PND--GCTWKGTLKEVBSCHGSCLGCPPLTCG---PACKGLURSERKEHHTBECPKRSCL 163
 Oy 177 SHCKSQVPMKLOKHEDTCPVCVVSCHPKCSVQTLRSLSAHLSBCVNAPSTGSKRY 236
 |||||:
 Db 164 QHCRAPCSHVLDVHYEV-CPKPLTC-DGCKKKPQPRETFQDHVRACSKRCVRCRHV 221
 Oy 237 GCYFGTQNIQKHAESA-SAVQVNLKREWNSLEKVKV-----LQONESVEKNKS 286
 |||||:
 Db 222 GCSEMVETBNLQDHELORLREHLL---LSSPLEAOASPTLNQVGPPELLQRCQLEQK- 278

OY	287	IQLSHNQCSFEIERQEMRLRNNESKILHLQRVIDSQAEKIKELDEKEIRPFRQNWEA	346	DR	InterPro: IPR003007; TRAF.
Db	279	IATFENIVQNLNRVTELEESVDKSAGQAARTNTGLESOLSRHQTLSDVHDIRLADMDFQ	312	DR	InterPro: IPR01293; Znf_TRAF.
OY	347	DSMKSSVSEIQNLNRVTELEESVDKSAGQAARTNTGLESOLSRHQTLSDVHDIRLADMDFQ	406	DR	InterPro: IPR01841; Znf_ring.
Db	313	-----KIEALSKVQOLE-----	343	DR	Pfam: PF00917; MATH_1.
Db	407	VLETASYNGVLINKIRDYRKRRQEAVMGKTLSLYSOPFYTGFGYMCARVYLNGDMCK	466	DR	Pfam: PF00917; zf_C3HC4_1.
Db	344	ELEVSTYDGVFIWKISDFTRKROEAVAGRTPAIFSPAFYTSRGYKMLCRYLNGDTGR	403	DR	Pfam: PF00917; MATH_1.
OY	467	GTHLSLFVFTIMRGYDALLPPWPKQYTLMLDQGSSRRHLGDAFKDPNNSFFKPKTGE	526	DR	Pfam: PF02176; zf_TRAF_2.
Db	404	GTHLSLFVFMKGPDNALIQLWPNTQYMLDH-NRREVIDAFRPDVWSSSTORPVSH	462	DR	SMART: SM00181; RING_1.
OY	527	MNTASGGCPVFAQVYLE-NGTYIKDDTFIKVIVDSL	564	DR	PROSITE: PS50089; ZF_RING_1; 2.
Db	463	MNTASGGCPVFAQVYLE-NGTYIKDDTFIKVIVDSL	501	DR	PROSITE: PS50145; ZF_TRAF_2.
RESULT 4				KW	Zinc-Finger; Coiled coil; Repeat.
TRA2_HUMAN				FT	FTN_FING
ID TRA2_HUMAN		STANDARD;	PRT;	FT	124
AC Q12933;			501 AA.	FT	180
DT 30-MAY-2000 (Rel. 39, Created)				FT	233
DT 15-JUN-2002 (Rel. 41, Last annotation update)				FT	299
DE TRAF receptor associated factor 2 (TRAFF) (Tumor necrosis factor type 2 receptor associated protein 3).				FT	348
DE Homo sapiens (Human).				FT	501
OS Homo sapiens (Human).				FT	365
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				FT	370
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				FT	375
OX NCBI_TaxID:9606;				FT	380
RN [1]				FT	385
RP MEDLINE=95366958; PubMed=7639698;				FT	390
RA Song H.Y.; Donner D.B.;				FT	395
RT "Association of a RING finger protein with the cytoplasmic domain of the human type-2 tumour necrosis factor receptor.";				FT	400
RL Biochem. J. 309: 825-829(1995).				FT	405
RN [2]				FT	410
RP SEQUENCE OF 201-501 FROM N.A.				FT	415
RX MEDLINE=94149371; PubMed=8069916;				FT	420
RA Rothe M.; Wong S.C.; Henseleit W.J.; Goeddel D.V.;				FT	425
RT "A novel family of putative signal transducers associated with the cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";				FT	430
RL Biochem. J. 309: 683-692(1994).				FT	435
CC OF THE 75 kDa TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND ACTIVATES NP-KAPPA-B.				FT	440
CC -I- SUBUNIT: HOMODIMER OR HETERO-DIMER OF TRAF1 AND TRAF2. THIS HETERO-COMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).				FT	445
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.				FT	450
CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.				FT	455
CC -I- SIMILARITY: CONTAINS 1 MATH/TRAFF DOMAIN.				FT	460
CC -I- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.				FT	465
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CC DR EMBL; U12597; AAA87706; 1; -				FT	475
DR Geno; HGNC:12032; TRAF2.				FT	480
DR MM: 601895; -.				FT	485
DR InterPro: IPR002003; MATH.				FT	490
RESULT 5				DR	InterPro: IPR003007; TRAF.
TRA1_HUMAN				DR	InterPro: IPR01293; Znf_TRAF.
ID TRA1_HUMAN		STANDARD;	PRT;	DR	InterPro: IPR01841; Znf_ring.
AC Q13077;			416 AA..	DR	Pfam: PF00917; zf_C3HC4_1.
DT 30-MAY-2000 (Rel. 39, Last sequence update)				DR	Pfam: PF00917; MATH_1.
DT 30-MAY-2000 (Rel. 39, Last sequence update)				DR	SMART: SM00181; RING_1.
Db 341	ONWEEADSMKSSVSEIQNLNRVTELEESVDKSAGQAARTNTGLESOLSRHQTLSDVHDIRLADMAD	400	DR	PROSITE: PS50089; ZF_RING_1; 2.	
Db 306	OHRLDDD-----KIEALSKVQOLE-----	337	DR	PROSITE: PS50145; ZF_TRAF_2.	
OY 401	MDLRFQVLETAWSYNGVLINKIRDYRKRRQEAVMGKTLSLYSOPFYTGFGYMCARVYLNGDMCK	460	DR	Zinc-Finger; Coiled coil; Repeat.	
Db 338	LEQKVRPFQACQGHRYCSFCLASIRLKQEAQIFSPAFYTSRGYKMLCRYLN	397	DR	FTN_FING	
OY 461	GDGMQKGTHSLSLFVFTIMRGYDALLPPWPKQYTLMLDQGSSRRHLGDAFKDPNNSF	520	DR	FTN_FING	
Db 398	GDGTGRTGTHSLFVFMKGPDNALIQLWPNTQYMLDH-NRREVIDAFRPDVWSSSTORPVSH	456	DR	FTN_FING	
OY 521	KKPTGEMMNTASGGCPVFAQVYLE-NGTYIKDDTFIKVIVDSL	564	DR	FTN_FING	
Db 457	QRPVNDMNTASGGCPVFSKMEAKNSYVRDDAIFIKAIVDLGL	501	DR	FTN_FING	

DE TNF receptor associated factor 1 (TRAFL) (Epstein-Barr virus-induced
DE protein 6).
GN TRAF1 OR EBI6
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TAXID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Lymphoma;
RX MEDLINE=5163092; PubMed=78559281;
RA Mostalas G., Birkenbach M., Yalamanchili R., VanArsdale T., Ware C., Kleff E.;
RA "The Epstein-Barr virus transforming protein LMP1 engages signaling
RT proteins for the tumor necrosis factor receptor family.";
RL 80:89-99(1995).
CC -I- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
OF THE 75 kDa TUMOR NECROSIS FACTOR RECEPTOR (TNF-R).
-I- SUBUNIT: HOMODIMER OR HETERO DIMER OF TRAF1 AND TRAF2. THIS
HETERO COMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS
PROTEINS 1 AND 2 (IAPS), TO RECRUIT THEM TO THE TUMOR NECROSIS
FACTOR RECEPTOR 2 (TNFR2).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- SIMILARITY: CONTAINS 1 MATH/TRAf DOMAIN.
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or send an email to license@lsb-sib.ch).
CC EMBL; U19201; AAAG62309.1; --.
DR Genebank HGNC:12031; TRAF1.
DR MIM: 601711; --.
DR InterPro: IPR002083; MATH.
DR InterPro: IPR003007; TRAF.
DR Pfam: PF00917; MATH; 1.
DR SMART: SM00061; MATH; 1.
KW Coiled coil.
FT DOMAIN 182 264 COILED COIL (POTENTIAL).
FT DOMAIN 269 354 MATH/TRAf.
SQ SEQUENCE 416 AA: 46163 MW: A956A123A40D284A CRC64;

Query Match 21.4%; Score 641.5; DB 1; Length 416;
Best Local Similarity 35.5%; Pred. No. 1e-31; Matches 126; Indels 103; Gaps 17;
Matches 165; Conservative 71; Mismatches 126; Indels 103; Gaps 17;

QY 137 KNECQFEELPCIRADCKEVKVLKDLRHDVKEACKYREATCSHCKSQVPMKLQKHEDDC 196
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 15 ENFPFGCPPTVQDPKRE-----RALCCAGCLENP----RNGEDQIC 54
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 197 PCVVVSCPHKCVSOTL-----LASLSAHLSECVAAPSTCSFKRYGVFGTNQQIK 248
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 55 P-----KCRCGDLQSISSPSRLRIQKEAH-PEVAEGIGCPPAGVGCSFKSPSVO 105
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 106 EHEVTSQTSNLNLIGENKQWAKRGGGLESGPMALBONLSDQLQAAVEAGDLEVDY 165
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 249 AHEASSAYOHVNLL---KEMW-----NSLEKKVSLQ_NESVERKNSQ-SLH 291
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 166 RAPOS-----ESQBE-----LALQHFM---KEKILAELEGKLRVF-----E 198
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 352 SVEISLQNRYTELESVDKSAGQAARTNGLGLESLSRH-----DQPLSVIDRLA 399
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 292 NQICSFETIEROKEMLRNNESKILHQLRVDSQAELKELDETRPPFRQNWEEADSMKS 351
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 166 RAPOS-----ESQBE-----LALQHFM---KEKILAELEGKLRVF-----E 198
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 352 SVEISLQNRYTELESVDKSAGQAARTNGLGLESLSRH-----DQPLSVIDRLA 399
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 199 NIVAVILKEVE-----ASHLALATSHOSLDRLRTLSLQRVVLQTLAQDAG 251
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 400 DMDLRFQVLETASYNGVLTWKDYKRKQAVMGKTLISLYSQPFITGYGKMCARVYL 459
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 252 KLEOSLRLMEEASDGTEFLWIKITVTRCHEEACGRVYLSSPAFTAKGYKLCLRLV 311
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 6
TRAf_MOUSE STANDARD: PRT: 409 AA.
ID_TRAf_MOUSE ID_TRAf_MOUSE PRT:
AC P39428; 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE TNF receptor associated factor 1 (TRAFL).
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 123-135 AND 390-402.
RX MEDLINE=54349371; PubMed=8069916;
RA Rothie M., Wong S.C., Henzel W.J., Goeddel D.V.;
CC "A novel family of putative signal transducers associated with the
cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL Cell 78:681-692(1994).
CC -I- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
OF THE 75 kDa TUMOR NECROSIS FACTOR RECEPTOR (TNF-R).
-I- SUBUNIT: HOMODIMER OR HETERO DIMER OF TRAF1 AND TRAF2. THIS
HETERO COMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS
PROTEINS 1 AND 2 (IAPS), TO RECRUIT THEM TO THE TUMOR NECROSIS
FACTOR RECEPTOR 2 (TNFR2).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- SIMILARITY: CONTAINS 1 MATH/TRAf DOMAIN.
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CC EMBL; L135302; AAC37663.1; --.
DR M6D; MGI:101836; Trafl.
DR InterPro: IPR002083; MATH.
DR InterPro: IPR003007; TRAF.
DR Pfam: PF00917; MATH; 1.
DR SMART: SM00061; MATH; 1.
KW Coiled coil.
FT DOMAIN 167 256 COILED COIL (POTENTIAL).
FT DOMAIN 260 347 MATH/TRAf.
SQ SEQUENCE 409 AA: 45464 MW: EBA7FEE5639FEDDF CRC64;

Query Match 21.4%; Score 640; DB 1; Length 409;
Best Local Similarity 35.5%; Pred. No. 1.3e-31; Matches 162; Indels 86; Gaps 15;
Matches 162; Conservative 72; Mismatches 136; Indels 86; Gaps 15;

QY 137 KNECQFEELPCIRADCKEVKVLKDLRHDVKEACKYREATCSHCKSQVPMKLQKHEDDC 196
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 9 ENFPQF--GCPPACQD-----PSEPVLCCTACLE---NLRDDERIC 48
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 197 PCVVVSCPHKCVSOTL-----LASLSAHLSECVAAPSTCSFKRYGVFGTNQQIK 256
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 49 PKCRADNLHPVSGSPITQE_KVH-SDVAEAEMCPAGYGCFSRGSPOSMOEHEATSQS 106
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 257 OHNL---LKEMW-----LEKKVSLQNESEVKNSQISLQNIQCSFEEI 301
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 107 SHYLLLAWLKEWKGSPCGNLGSAPMALERNSELQ-----LQAAVEATGDELVC 157

RN [3]
 RF SEQUENCE FROM N.A..
 RC STRAINE-BALD/C;
 RX MEDLINE=98010627; PubMed=9346933;
 RA Thesis, I., Tryggestad, K.;
 RT "primary structure, developmental expression, and immunolocalization
 of the murine laminin alpha4 chain";
 RL J. Biol. Chem. 272:27862-27868(1997).
 RN [4]
 RR SEQUENCE OF 836-1105 FROM N.A.
 RC STRAIN-EICR; TISSUE=placenta;
 RX MEDLINE=97296337; PubMed=9151674;
 RA Miner, J.H., Patton, B.L., Lentz, S.I., Gilbert, D.J., Snider, W.D.,
 RA Jenkins, N.A., Copeland, N.G., Sanes, J.R.;
 RT "The laminin alpha chains: expression, developmental transitions, and
 chromosomal locations of alpha1-5, identification of heterotrimeric
 laminins 8-11, and cloning of a novel alpha3 isoform";
 RL J. Cell Biol. 137:685-702(1997).
 RN [5]
 RR SEQUENCE OF 1467-1691 FROM N.A.
 RC TISSUE=placenta;
 RX MEDLINE=97178457; PubMed=9034910;
 RA Lentz, S.I., Miner, J.H., Sanes, J.R., Snider, W.D.;
 RT "Distribution of the ten known laminin chains in the pathways and
 targets of developing sensory axons";
 RL Comp. Neurol. 378:547-561(1997).
 CC -I- FUNCTION: Binding to cells via a high affinity receptor, laminin
 19 thought to mediate the attachment, migration, and organization
 of cells into tissues during embryonic development by interacting
 with other extracellular matrix components.
 CC -I- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 different polypeptide chains (alpha, beta, gamma), which are bound
 to each other by disulfide bonds into a cross-shaped molecule
 comprising one long and three short arms with globules at each
 end.
 CC -I- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
 MEMBRANES (MAJOR COMPONENT).
 -I- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN PERIPHERAL NERVES,
 CARDIAC MUSCLE, FAT, DERMIS, LUNG STROMA, AORTIC ENDOTHELIUM,
 ENDOCARDIUM AND ENDOTHELIUM OF BLOOD VESSELS IN SKIN AND BRAIN.
 -I- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
 WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
 -I- DOMAIN: DOMAIN G IS GLOBULAR.
 CC -I- SIMILARITY: CONTAINS 3-5 LAMININ EGF-LIKE DOMAINS.
 CC -I- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR HSSP; P02468; 1KLO.
 DR EMBL; U58950; AAB41840.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR021049; Laminin-EGF.
 DR InterPro; IPR01791; Laminin_G.
 DR Pfam; PF00053; laminin_EGF; 3.
 DR Pfam; PF00054; laminin_G; 4.
 DR SMART; SM0181; EGF; 3.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
 KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;

Query	Match	Score	Length
Best Local Similarity	5.6%	168	1
	Pred. No.	0.014	
SEQUENCE	19.6%	1816	1816
FT SIGNAL	1	24	POTENTIAL.
FT CHAIN	25	1816	LAMININ ALPHA-4 CHAIN.
FT DOMAIN	82	1811	LAMININ EGF-LIKE 1.
FT DOMAIN	132	186	LAMININ EGF-LIKE 2.
FT DOMAIN	187	240	LAMININ EGF-LIKE 3.
FT DOMAIN	241	255	LAMININ EGF-LIKE 4 (INCOMPLETE).
FT DOMAIN	256	825	DOMAIN II AND I.
FT DOMAIN	826	1030	LAMININ G-LIKE 1.
FT DOMAIN	1042	1222	LAMININ G-LIKE 2.
FT DOMAIN	1229	1397	LAMININ G-LIKE 3.
FT DOMAIN	1462	1633	LAMININ G-LIKE 4.
FT DOMAIN	1640	1813	LAMININ G-LIKE 5.
FT DOMAIN	431	523	COILED COIL (POTENTIAL).
FT DOMAIN	556	604	COILED COIL (POTENTIAL).
FT DOMAIN	675	717	COILED COIL (POTENTIAL).
FT DOMAIN	770	799	COILED COIL (POTENTIAL).
FT SITE	717	719	CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID	82	91	BY SIMILARITY.
FT DISULFID	84	98	BY SIMILARITY.
FT DISULFID	101	110	BY SIMILARITY.
FT DISULFID	113	129	BY SIMILARITY.
FT DISULFID	132	146	BY SIMILARITY.
FT DISULFID	134	155	BY SIMILARITY.
FT DISULFID	157	166	BY SIMILARITY.
FT DISULFID	169	184	BY SIMILARITY.
FT DISULFID	187	202	BY SIMILARITY.
FT DISULFID	212	221	BY SIMILARITY.
FT DISULFID	224	238	BY SIMILARITY.
FT DISULFID	266	266	BY SIMILARITY.
FT DISULFID	269	269	INTERCHAIN (PROBABLE).
FT CARBOHYD	104	104	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	215	571	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	308	574	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	333	574	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	458	550	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	550	550	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	571	571	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	574	574	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	631	631	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	639	639	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	735	735	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	751	751	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	754	754	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	780	780	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	803	803	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	1088	1088	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	1283	1283	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	1361	1361	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT	8	8	C > S (IN REF. 2).
FT CONFLICT	18	18	C > Y (IN REF. 2).
FT CONFLICT	248	248	C > R (IN REF. 3).
FT CONFLICT	297	297	G > A (IN REF. 3).
FT CONFLICT	431	433	THR > HPS (IN REF. 2).
FT CONFLICT	679	679	S > C (IN REF. 3).
FT CONFLICT	703	703	D > G (IN REF. 2).
FT CONFLICT	706	706	N > H (IN REF. 2).
FT CONFLICT	728	728	K > R (IN REF. 2).
FT CONFLICT	730	730	F > I (IN REF. 2).
FT CONFLICT	779	779	R > G (IN REF. 1; AA SEQUENCE).
FT CONFLICT	810	810	R > S (IN REF. 3).
FT CONFLICT	865	865	AEP > Q (IN REF. 2).
FT CONFLICT	935	936	K > E (IN REF. 3).
FT CONFLICT	970	970	L > V (IN REF. 3).
FT CONFLICT	1132	1132	H > R (IN REF. 2).
FT CONFLICT	1200	1200	F > I (IN REF. 2).
FT CONFLICT	1382	1382	D > A (IN REF. 2).
FT CONFLICT	1414	1414	NS > EF (IN REF. 1).
FT CONFLICT	1489	1489	A > S (IN REF. 2).
FT CONFLICT	1816	1818	B49C45F3A4999DB CRC64;

Matches 105; conservative 79; Mismatches 201; Indels 152; Gaps 24;

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AP000058; BAA790201; -
 DR Interpro; IPR003439; ABC transporter.
 DR Interpro; IPR003405; SMC_C.
 DR Interpro; IPR003395; SMC_N.
 DR Pfam; PF02463; SMC_C; 1.
 DR Pfnam; PF02483; SMC_C; 1.
 DR DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
 DR NP_BIND .
 FT DOMAIN .
 FT SEQUENCE .
 Query Match Similarity 5 %; Score 164; DB 1; Length 919;
 Best Local Similarity 211%; Pred. No. 0.011; Mismatches 176; Indels 114; Gaps 16;
 Matches 98; Conservative 77; Mismatches 176; Indels 114; Gaps 16;
 Sequence 919 AA; 104138 MW; 7BFA80EB601B9DD CRC64;

QY 248 KHEAASSAVOHYNLKLKMSNSLEKKVSLQHNSVERKNKSIOSSHNOICSEFIEE --- 302

Db 293 SVSSGAAAHRYNDMNSTIHLRTRISERENQYTLRKIQINNSNENTLSLPPDVSGHLK 352

QY 303 ---RQEMLRNNE ---KILHQVQDSDQAEKUKELDEKEIRPFRQNWE --- 344

Db 353 GSQASRKGMLVKEKESMOTIDQATHQEQAHNMKDQEINSKMLYGENOELGPPIAEK 412

QY 345 -BADSMKSSVSLSQNRVTELESVDSAGQAARNGLSOLSRHDQTSVYHDIRLADM 402

Db 413 LVIQAKMLETISRSQPFLTHRELVEADEQELLSQAENWQRNLHNDTRSLFPVVQLEQD 472

QY 403 ------LRFQVLETFASYNGVLWIKROYKR ---IKQEAWMGKTSL 439

Db 473 DYNAKLSDLQESIINOALDHVRDAEDMINRATTFKORDHEKOHERVKEOMEVGASLM 529

QY 193 DTDCPCVWVSPHCKSVQTLR -SELSAHLSCVNAPSTCSFKRYGVFOQTNQTKH 250

Db 518 -----IELLSLRNQLEBGLE-----LGFOQPEDLAKE 547

QY 251 EASSAV-QVNLIKESNSLEKKVSLQHNSVERKNKSIOSSHNOICSEFIEE 305

Db 548 QKLMRLENLEELRKLENSELEKKVSLQHNSVERKNKSIOSSHNOICSEFIEE 603

QY 306 EMLRNNESHILHQVQDSDQAEKU --- 335

Db 604 EKLTKLSSSEKKLERMLVSKAEDLATRIGITAYRSLDLLEKAREALELEGVDKELSAERR 663

QY 336 IRPFRNNHEADSNKSSVSLSQNRVTELESVDSAGQAARNGLSOLSRHDQTSVYH 395

Db 664 LEEARRLKKEAKLWKWEAQMRLEELAEKKERLKVSEIEARKEVONTLAED 723

QY 395 IRLADMDFRFQVLETFASYNGVLWIKROYKR ---IKQEAWMGKTSL 440

Db 724 DRISRIDRENGELQT-----RIREMKSRT -ASGEDEALKY 757

RESULT 9

RA50_ADRPE STANDARD; PRT; 919 AA.

AC QYFZL; 16-OCT-2001 (Rel. 40, Created)
 AC QYFZL; 16-OCT-2001 (Rel. 40, Last sequence update)
 AC QYFZL; 16-OCT-2001 (Rel. 40, Last annotation update)

DR DNA double-strand break repair rad50 Atbase.

DR RAD50 OR APE010.

OS Aeropyrum pernix.

OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;

OC Desulfurococcaceae; Aeropyrum.

NCBI_TAXID=56636;

[1]

RP SEQUENCE FROM N.A.

RC STRAINKL;

RK MEDLINE=99310339; PubMed=10382966;

RA Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushida N., Ouchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.,
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101 (1999).

CC -!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
 rad50/mre11 complex possesses single-strand endonuclease activity.
 CC and Atp-dependent double-strand-specific exonuclease activity.
 CC Rad50 provides an Atp-dependent control of mre11 by unwinding
 CC and/or repositioning DNA ends into the mre11 active site (By
 CC similarity).

CC -!- SUBUNIT: Forms a complex with mre11 (By similarity).

CC -!- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.

CC

RESULT 10

2147_MOUSE STANDARD; PRT; 634 AA.

AC Q61510; 16-OCT-2001 (Rel. 40, Created)
 AC Q61510; 16-OCT-2001 (Rel. 40, Last sequence update)
 AC Q61510; 15-JUN-2002 (Rel. 41, Last annotation update)

DR Zinc finger protein 147 (tripartite motif protein 25) (Estrogen
 DE responsive finger Protein) (Efp).

DE ZNF147 OR TRIM25 OR zfp147 OR Efp.

GN Mus musculus mouse.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TAXID=10090;

RP SEQUENCE FROM N.A.

RC TISSUE=Uterus; Ovary, and Placenta;
 RX MEDLINE=9602535; PubMed=792654;
 RA Orimo A., Inoue S., Ikeda K., Noji S., Muramatsu M.;
 RT "Molecular cloning, structure, and expression of mouse estrogen-
 responsive finger protein Efp. Co-localization with estrogen receptor
 mRNA in target organs."
 RT RLU J. Biol. Chem. 270:24405-24413(1995).
 CC -I- FUNCTION: MEDIATES ESTROGEN ACTION IN VARIOUS TARGET ORGANS.
 CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 EMBL; D63902; BAA0941.1; --.
 DR MGD; MGI; I02749; Trin25.
 DR InterPro; IPR01870; Gamma_carboxylase.
 DR InterPro; IPR01877; SPRY_domain.
 DR InterPro; IPR003878; SPRY_domain.
 DR InterPro; IPR01841; Znf_fing.
 DR Pfam; PF00097; zf-C2HC4; 1.
 DR SMART; SM0018; SPRY; 1.
 DR SMART; SM00449; SPRY; 1.
 DR PROSITE; PS00518; ZF_RING_1; 1.
 KW PROSITE; PS50089; ZF_RING_2; 1.
 FT Zinc-finger; Coiled coil.
 FT ZN_FING 13 54 RING-TYPE
 FT DOMAIN 215 305 COILED COIL (POTENTIAL).
 FT DOMAIN 514 631 SPRY.
 SEQUENCE 634 AA; 71772 MW; 6695C99DE2832511 CRC64;
 Query Match 5.4%; Score 161; DB 1; Length 634;
 Best Local Similarity 18.5%; Pred. No. 0.01; Gaps 17;
 Matches 75; Conservative 65; Mismatches 130; Indels 136; Gaps 17;
 SQ .48 DKVKECEKRLVCLNPOTECCRRCFSCMALLSSSP--KCTACQESTIKDKVFKDNCC 105
 :|:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 9 EELSCSVCYCLELPKEPVTPCGHNFCTSLCDETWVQGPPYPRCPOCR-----KVYQ--V 59
 QY 106 KRETLALOVYC-----RNEGRGCAEQILTGHLLVHK-NECQ 141
 :|:|||:|||:|||:|||:|||:|||:|||:
 Db 60 RPOLOKNTMCAVVEQELQAEQARTPYDDWTPPARPSASSATQAFACDICTLTAKTC- 118
 142 FEELPCLRADCKEV-----LRKDLDHVKEAC---KIREATCSHKSQVP 184
 :|:|||:|||:|||:|||:|||:
 Db 119 --LVCMASFCQBHLRPHEDSAFQDHPLQSQSPIDLRKCTOHNLREFFCP----- 168
 185 MIKLOKHEDPTCPVVVSCPK--CSVTOLLRSLSAHLSECUNAPSTCSKRRGGVFQGT 243
 :|:|||:|||:|||:|||:|||:
 Db 169 -----EYKLNKRLTMHSHTNGATKALEYRSKOCVQDSMKR 235
 :|:|||:|||:|||:
 Db HSSP; P03437; 1HM.
 DR InterPro; IPR002928; Myosin-tail.
 DR Pfam; PF0156; Myosin_tail; 1.
 KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
 ATP-binding; Multigene family.
 DR NON_TER 1
 FT DOMAIN <1 1102 COILED COIL (POTENTIAL).
 FT CONFLICT 65 65 A -> T (IN REF. 1).
 FT CONFLICT 92 92 V -> A (IN REF. 1).
 FT CONFLICT 113 114 CS -> FAL (IN REF. 1).
 FT CONFLICT 135 135 H -> Q (IN REF. 1).
 FT CONFLICT 185 185 T -> R (IN REF. 1).
 SQ SEQUENCE 1102 AA; 128008 MW; 22336680049825DC CRC64;
 Query Match 5.3%; Score 157.5; DB 1; Length 1102;
 Best Local Similarity 20.1%; Pred. No. 0.034; Gaps 21;
 Matches 102; Conservative 85; Mismatches 184; Indels 137; Gaps 21;

RESULT 11
 ID MTSC_CHICK STANDARD; PRT; 1102 AA.

QY	14	OPNPPKPKLQDGRGAGSVVPEFOGGYKEVKTVTEDKYCKEKGRLVLPNPQTCGHRFE	73	CC	-I - SUBCELLULAR LOCATION: Type I membrane protein.
Db	591	QEDMMIDLERANSAAASLKDQKRGF-DKINDNRKQYESQAEI-----EASOKEAR	641	CC	-I - ALTERNATIVE PRODUCTS: 2 ISOMORFS, THE BETA AND BETA' SUBUNITS, DIFFER IN THEIR N-TERMINUS DUE TO DIFFERENTIAL PROMOTER USAGE AND ALTERNATIVE SPLICING.
OY	74	SCMAALLSSSPKPTACQPSIIKKVFKDNCCRELLALQVICVRNEGRGCAEQLTGHLL	133	CC	-I - TISSUE SPECIFICITY: THE BETA-SUBUNIT IS EXPRESSED IN KIDNEY, INTESTINAL BRUSH BORDERS, AND SALIVARY DUCTS. THE BETA'-ISOFORM HAS BEEN FOUND IN CARCINOMA CELLS.
Db	642	SLSLEFLKLNN---AYEETH-L-DHL---ETAKRENKLNQ---EESDLTNQISSEGKNN	688	CC	-I - INDUCTION: By retinoic acid.
Db	134	VH-----LKNECOFF-----ELPCLRADCKEVLRKD-	160	CC	-I - PTM: THIS PROTEIN UNDERGOES PROTEOLYTIC PROCESSING. BOTH FORMS ARE GLYCOSYLATED.
OY	689	LHETEKVKVKQVEQEYVQALEBAAEGALEHEESKTIRFQELSLQSKADFERKLAEKDEE	748	CC	-I - SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
QY	161	--LADHVVERACKYREACT-SHCKSQVMKQKHEPDPCPVWVSCPH-----	205	CC	-I - SIMILARITY: CONTAINS 1 MAM DOMAIN.
Db	749	MQNIRRNOQTIDSLSQSTLDSEARSNEAIRLKMKMGDLNEMEIQLSHANRHAATKS	808	CC	-I - SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
OY	206	KCSVTQTLSEELS-----AHISECWNPSTCSFKRKGCVVOGTNOOKA-----	249	CC	-I - INDUCTION: By retinoic acid.
Db	809	ARGHQIQK-TLOVQDLDIGHUNEDKBLQAVSDRRNN-LIQSELDELALLDQTERARK	866	CC	-I - PTM: THIS PROTEIN UNDERGOES PROTEOLYTIC PROCESSING. BOTH FORMS ARE GLYCOSYLATED.
OY	250	--HEASSAVWHNLKEMNS-----LEKKVSLQNESEVKNSIOSLHNQTCSEFI	299	CC	-I - TISSUE SPECIFICITY: THE BETA-SUBUNIT IS EXPRESSED IN KIDNEY, INTESTINAL BRUSH BORDERS, AND SALIVARY DUCTS. THE BETA'-ISOFORM HAS BEEN FOUND IN CARCINOMA CELLS.
Db	867	LAERHLLEATEYVNLLHTNTSLINOKKLGSDISMQNEESTOECRNEAQAKKATT	926	CC	-I - SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
OY	300	EIEQKEMPRANNHQLHQVIDSQAEKLLDKLDEKFPRFRQWEADS-----KSSVE	354	CC	-I - SIMILARITY: CONTAINS 1 MAM DOMAIN.
Db	927	DAAMMAEELUKKEQDTSAHLEMRKMKNMQTIDQIQLR-----DEREQIAKGGRKQIO	979	CC	-I - INDUCTION: By retinoic acid.
OY	355	SLQNRVTELES-----VDKSAGQARNTGLESOLSRHDQTLSYHDIDLADM	403	CC	-I - PTM: THIS PROTEIN UNDERGOES PROTEOLYTIC PROCESSING. BOTH FORMS ARE GLYCOSYLATED.
Db	980	KLESVRYLNELENELNERNMSAQKARKFERRIKELTYQSEEDKRNL-----RMQDLD	1035	CC	-I - TISSUE SPECIFICITY: THE BETA-SUBUNIT PRECURSOR IS EXPRESSED IN KIDNEY, INTESTINAL BRUSH BORDERS, AND SALIVARY DUCTS. THE BETA'-ISOFORM USES A DIFFERENT PROMOTER.
OY	404	RFOVLETASYNGLIWKIRDYKRKREA	431	CC	-I - SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
Db	1036	KLQL-----KVKSYKHOEEA	1051	CC	-I - INDUCTION: By retinoic acid.
RESULT 12					
MEPB_MOUSE				DR	HSPB; P28822; ITAF.
ID	MEPB_MOUSE	STANDARD;	PRT;	DR	MEOPS; M12_004; -.
AC	Q61847;			DR	MGB; M9664; Mepib.
DT	01-NOV-1997 (Rel. 35, Created)			DR	InterPro; IPR001506; Astacin.
DT	01-NOV-1997 (Rel. 35, Last sequence update)			DR	InterPro; IPR000561; EGF-like.
DE	Meprin A beta-subunit precursor (EC 3.4.24.18) (Endopeptidase-2).			DR	InterPro; IPR000998; MAM_domain.
MEPB_OR_MEP-1B				DR	InterPro; IPR002083; MATH.
MUS	MUSCULUS (Mouse)			DR	InterPro; IPR003007; TRAF.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; MUS.			DR	InterPro; IPR000130; Zn_Mipeptidase.
NCBI_TAXID-10090;				DR	pfam; PF00917; MATH; 1.
OX				DR	pfam; PF00917; MATH; 1.
RN	[1]	SEQUENCE FROM N A., AND PARTIAL SEQUENCE.		DR	pfam; PF01400; Astacin; 1.
RT	SEQUENCE FROM N A., AND PARTIAL SEQUENCE.			DR	PRINTS; PRO0480; ASTACIN.
RC	TISSUE-Kidney;			DR	PRINTS; PRO00020; MAMDOMAIN.
RR	Jenkins N.A., Bond J.S., Jiang W., Copeland N.G., Gilbert D.J., Gorbea C.M., Marchand P., Jiang R., Medline#9402651; PubMed#8407940;			DR	SMART; SM00181; EGF; 1.
RT	"Cloning, expression, and chromosomal localization of the mouse meprin beta subunit,"			DR	SMART; SM00137; MAM; 1.
RT	J. Biol. Chem. 268:21035-21043(1993).			DR	SMART; SM00061; MATH; 1.
RR	[2]	SEQUENCE FROM N A. (ISOFORM BETA').		DR	PROSITE; PS00143; ZINC_PROTEASE; 1.
RR	TISSUE-Kidney;			DR	PROSITE; PS00740; MAM_1; 1.
RR	"A novel meprin beta' mRNA in mouse embryonal and human colon carcinoma cells,"			DR	PROSITE; PS50060; MAM_2; 1.
RR	J. Biol. Chem. 271:2271-2278(1996).			DR	PROSITE; PS0022; EGF_1; FALSE_NEG.
RR	-- CATALYTIC ACTIVITY: Hydrolysis of protein and peptide substrates preferentially on carboxyl side of hydrophobic residues.			DR	PROSITE; PS01186; EGF_2; FALSE_NEG.
RR	-! COFACTOR: Binds 1 ZINC ION.			FT	ZYMOGEN; Signal; EGF-like domain; Alternative splicing.
RR	-! SUBUNIT: HETEROOTRAMER OF TWO ALPHA AND TWO BETA SUBUNITS WHICH IS FORMED BY THE NON-COVALENT ASSOCIATION OF TWO DISULFIDE-LINKED HETERODIMERS.			FT	SIGNAL; 20 POTENTIAL.
RR	TISSUE=Kidney;			FT	BY SIMILARITY.
RR	MEDLINE#9614721; PubMed#8567689;			FT	MEPRIN A BETA-SUBUNIT.
RR	Dietrich J.M., Bond J.S., Jiang W.;			FT	EXTRACELLULAR (POTENTIAL).
RR	"A novel meprin beta' mRNA in mouse embryonal and human colon carcinoma cells,"			FT	POTENTIAL.
RR	J. Biol. Chem. 271:2271-2278(1996).			FT	CYTOSPLASMIC (POTENTIAL).
RR	-- CATALYTIC ACTIVITY: Hydrolysis of protein and peptide substrates preferentially on carboxyl side of hydrophobic residues.			FT	METALLOPROTEASE.
RR	-! COFACTOR: Binds 1 ZINC ION.			FT	MAM.
RR	-! SUBUNIT: HETEROOTRAMER OF TWO ALPHA AND TWO BETA SUBUNITS WHICH IS FORMED BY THE NON-COVALENT ASSOCIATION OF TWO DISULFIDE-LINKED HETERODIMERS.			FT	EGF-LIKE.
RR	RR			FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
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RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR				FT	BY SIMILARITY.
RR				FT	N-LINKED (GLCNAC . . .) (POTENTIAL).
RR				FT	ZINC (CATALYTIC) (BY SIMILARITY).
RR		</td			

FT	CARBOHYD	593	593	N-LINKED (GLCNAC, .) (POTENTIAL).	CC
FT	VARSPLIC	1	27	MDSRQHQPFLVFAFPFLASGLPAPKEK -> MNSTAGPASR	CC
FT	SEQUENCE	704 AA;	79548 MW;	SRSFCKNLK5KAPRQDGMMMFQG (IN ISOFORM BFR')	CC
FT	SEQUENCE	704 AA;	79548 MW;	BFR')	CC
CC	CC	CC	CC	entities requires a license agreement (See http://www.istb-sib.ch/announcements) or send an email to license@istb-sib.ch).	CC
CC	DR	DR	DR	ERBL; Z70690; CRA94634.1; -.	CC
CC	KW	KW	KW	Hypothetical protein	CC
CC	SQ	SQ	SQ	SEQUENCE 1957 AA; 222785 MW; 3F480CA06171D9DA CRC64;	CC
Query Match	5.1%	Score 151.5;	DB 1;	Length 704;	
Best Local Similarity	25.1%	Pred. No. 0.046;			
Matches	54;	Conservative	38;	Mismatches 56;	
				Indels 67;	Gaps 11;
QY	391	LSDHDILRLADDMLRFQVLETASYNGVLWKIRDKRKQEAVMGKTLISLISOPPFYQFG	450	NLINKED (GLCNAC, .) (POTENTIAL).	
Db	416	LSIDDDINLSETRCPHH-----IWHIQNF----TQIUGQDPISVSSPFVSK-G	459	the European Bioinformatics Institute. There are no restrictions on 1	
QY	451	YKMCARVYLNGDGKGKTHLSSLFVFVIMRGYEDALLPNWPKF-OKVTLIMLDQ-----	500	use by non-profit institutions as long as its content is in no way	
Db	460	YAF---QIMD--LRISTNVGIVFHLLSGANDRQLQNPWPQWATMILQNDQDIRQRMF	514	modified and this statement is not removed. Usage by and for commercial	
QY	501	-----GS-----SRRHGDAAFKRPDPNSSSKFPTGEWNIAASGPVVAQ	539	entities requires a license agreement (See http://www.istb-sib.ch/announcements) or send an email to license@istb-sib.ch).	
Db	515	NQRSTTDPTMTSDNGSYFWDRPSKVGVTFVDE--PNGTOFSR----GIGYGTTFVTR	566		
QY	540	TVLNGTYIKDDTIFKIVD-----TSDLPDP	567		
Db	567	ERLKSRREFIKGGDDIYILLVEDISHLNSTSAVPDP	601		
RESULT 13					
YD86-SCHPO					
ID					
YD86-SCHPO					
STANDARD:					
PRT:	1957 AA.				
AC	010411;				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Hypothetical protein CIP3.06C in chromosome 1.				
SPAC13.06C.					
OS	Schizosaccharomyces pombe (Fission yeast).				
OC	Fungi; Ascomycota; Schizosaccharomycetes;				
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;				
OX	NCBI_TAXID=4896;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAN=97;				
RX	MEDLINE=21848401; PubMed=11859360;				
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,				
RA	Sgouros J., Peat N., Haynes J., Baker S., Basham D., Bowman S.,				
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,				
RA	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,				
RA	Gentles S., Goode A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,				
RA	Holloway S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,				
RA	James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,				
RA	Mooney P., Moule S., Mundall K., Murphy L., Niblett D., Odell C.,				
RA	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinovitsch E.,				
RA	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,				
RA	Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,				
RA	Taylor K., Taylor R.G., Tilvey A., Walsh S.V., Warren T., Whitehead S.,				
RA	Woodward J., Volckaert G., Aert R., Robben J., Grymonpre B.,				
RA	Weltens I., Vanstreels E., Rieger M., Schaeffer M., Mueller-Auer S.,				
RA	Gabel C., Fuchs M., Fritz C., Hoizer E., Moestl D., Hilbert H.,				
RA	Borzym K., Lanier I., Beck H., Lehach H., Reinhardt R., Pohl T.M.,				
RA	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,				
RA	Goffeau A., Cadieu E., Deaneo S., Gloux S., Delaure V., Mottier S.,				
RA	Goffeau F., Avies S., Xiang Z., Hunt C., Moore K., Hurst S.M.,				
RA	Lucas M., Rochet M., Gaillardin C., Taillada V.A., Garzon A., Thode G.,				
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,				
RA	Domínguez A., Revuelta J.L., Moreno S., Armstrong J., Borsburg S.L.,				
RA	Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,				
RA	Shpakowski G.V., Ussey R., Barrell B.G., Nurse P.,				
RA	"The genome sequence of Schizosaccharomyces pombe.";				
RA	Nature 415:871-880(2002).				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				

[2]	SEQUENCE FROM N.A.	FT	SIGNAL	1	POTENTIAL.
RC	TISSUE-Heart;	FT	CHAIN	24	LAMININ ALPHA-4 CHAIN.
RX	MEDLINE=9754279; PubMed=9310354;	FT	DOMAIN	1816	LAMININ EGF-LIKE 1.
RA	Richards A.J., Lucarini C., Pope F.M.;	FT	DOMAIN	82	LAMININ EGF-LIKE 2.
RT	The structural organisation of LAMA4, the gene encoding laminin alpha4. ";	FT	DOMAIN	132	LAMININ EGF-LIKE 3.
RT	Eur. J. Biochem. 248:15-23(1997).	FT	DOMAIN	187	LAMININ EGF-LIKE 4 (INCOMPLETE).
RL	Pope F.M.;	FT	DOMAIN	240	LAMININ EGF-LIKE 4 DOMAIN II AND I.
RN	"Localization of the gene (LAMA4) to chromosome 6q21 and isolation of a partial cDNA encoding a variant laminin A chain.";	FT	DOMAIN	255	LAMININ G-LIKE 1.
RP	SEQUENCE OF 236-1816 FROM N.A.	FT	DOMAIN	825	LAMININ G-LIKE 2.
RC	TISSUE-Heart;	FT	DOMAIN	826	LAMININ G-LIKE 3.
RL	Genomics 22:237-239(1994).	FT	DOMAIN	1028	LAMININ G-LIKE 4.
RX	MEDLINE=95048381; PubMed=7959779;	FT	DOMAIN	1462	LAMININ G-LIKE 5.
RA	Richards A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leversta M.A., Pope F.M.;	FT	DOMAIN	1633	COLLED COIL (POTENTIAL).
RA	"Localization of the gene (LAMA4) to chromosome 6q21 and isolation of a partial cDNA encoding a variant laminin A chain.";	FT	DOMAIN	1640	LAMININ EGF-LIKE 1.
RL	Genomics 22:237-239(1994).	FT	DOMAIN	313	LAMININ EGF-LIKE 2.
RX	SEQUENCE OF 66-1816 FROM N.A.	FT	DOMAIN	396	LAMININ EGF-LIKE 3.
RA	Tubby B.;	FT	DISULFID	466	LAMININ G-LIKE 4 (POTENTIAL).
RL	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.	FT	DISULFID	521	COLLED COIL (POTENTIAL).
CC	-!- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.	FT	DISULFID	101	COLLED COIL (POTENTIAL).
CC	-!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end.	FT	DISULFID	110	COLLED COIL (POTENTIAL).
CC	-!- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).	FT	DISULFID	113	COLLED COIL (POTENTIAL).
CC	-!- TISSUE SPECIFICITY: IN ADULT, STRONG EXPRESSION IN HEART, LUNG, OVARY, SMALL AND LARGE INTESTINES, PLACENTA, LIVER; WEAK OR NO EXPRESSION IN SKELETAL MUSCLE, KIDNEY, PANCREAS, TESTIS, PROSTATE, BRAIN - HIGH EXPRESSION IN FETAL LUNG AND KIDNEY. EXPRESSION IN FETAL AND NEWBORN TISSUES IS OBSERVED IN CERTAIN MESENCHYMAL CELLS IN TISSUES SUCH AS SMOOTH MUSCLE AND DERMIS.	FT	DISULFID	129	COLLED COIL (POTENTIAL).
CC	-!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.	FT	DISULFID	132	BY SIMILARITY.
CC	-!- DOMAIN: DOMAIN G IS GLOBULAR.	FT	DISULFID	146	BY SIMILARITY.
CC	-!- SIMILARITY: CONTAINS 3-5 LAMININ EGF-LIKE DOMAINS.	FT	DISULFID	155	BY SIMILARITY.
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	DISULFID	157	BY SIMILARITY.
CC	-!- CAUTION: GENE LAMA4 WAS FORMERLY CALLED LAMA3.	FT	DISULFID	166	BY SIMILARITY.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	FT	DISULFID	184	BY SIMILARITY.
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	DISULFID	187	BY SIMILARITY.
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	DISULFID	202	BY SIMILARITY.
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	DISULFID	209	BY SIMILARITY.
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	DISULFID	212	BY SIMILARITY.
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	DISULFID	221	BY SIMILARITY.
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	DISULFID	238	BY SIMILARITY.
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	DISULFID	266	INTERCHAIN (PROBABLE).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	DISULFID	269	INTERCHAIN (PROBABLE).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	104	(POTENTIAL).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	215	(POTENTIAL).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	308	(POTENTIAL).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	458	(POTENTIAL).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	524	(POTENTIAL).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	550	(POTENTIAL).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	571	(POTENTIAL).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	574	(POTENTIAL).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	631	(POTENTIAL).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	639	(POTENTIAL).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	735	N-LINKED (GLCNAC. . .)
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	751	(POTENTIAL).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	754	N-LINKED (GLCNAC. . .)
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	780	(POTENTIAL).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	803	N-LINKED (GLCNAC. . .)
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	1085	(POTENTIAL).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	1281	N-LINKED (GLCNAC. . .)
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	1359	(POTENTIAL).
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	1411	N-LINKED (GLCNAC. . .)
CC	-!- SIMILARITY: CONTAINS 5 LAMININ LIKE DOMAINS.	FT	CARBOHYD	143	(POTENTIAL).
DR	EMBL: S78569; AAC34635_1; -;	FT	CONFFLICT	143	A -> P (IN REF. 1).
DR	EMBL: X91171; CAA2596_1; -;	FT	CONFFLICT	178	L -> P (IN REF. 1).
DR	EMBL: Y14240; CAA74636_1; -;	FT	CONFFLICT	265	G -> GMDCPPTS (IN REF. 4).
DR	EMBL: X76939; CAA54258_1; -;	FT	CONFFLICT	276	D -> A (IN REF. 4).
DR	EMBL: 29289; CAB6553_1; -;	FT	CONFFLICT	491	Y -> H (IN REF. 2 AND 3).
DR	HSSP: P02468; KLO Genew; HGNC:6484; LAMA4. MIM: 600133; DR	FT	CONFFLICT	1057	T -> P (IN REF. 1).
DR	InterPro: IPR002049; Laminin_EGF.	FT	CONFFLICT	1110	SR -> GGP (IN REF. 4).
DR	InterPro: IPR001791; Laminin_G.	FT	CONFFLICT	1112	SQ -> GGP (IN REF. 4).
DR	Pfam: PF00053; laminin_EGF; 6.	FT	SEQUENCE	1816 AA;	04E9AF379A0F4A4D CRC64;
DR	Pfam: PF00054; laminin_G; 6.	FT	SEQUENCE	1816 AA;	04E9AF379A0F4A4D CRC64;
DR	SMART: SM02022; lamG; 5.	FT	SEQUENCE	1816 AA;	04E9AF379A0F4A4D CRC64;
DR	PROSITE: PS00022; EGF_1; UNKNOWN_1.	FT	SEQUENCE	1816 AA;	04E9AF379A0F4A4D CRC64;
DR	PROSITE: PS01248; LAMININ_TYPE_EGF; 3.	FT	SEQUENCE	1816 AA;	04E9AF379A0F4A4D CRC64;
DR	PROSITE: PS50025; LAM_G_DOMAIN; 5.	FT	SEQUENCE	1816 AA;	04E9AF379A0F4A4D CRC64;
KW	Glycoprotein; basement membrane; Extracellular matrix; Signal; Cell adhesion; Repeat; EGFLike domain; Coiled coil.	FT	SEQUENCE	1816 AA;	04E9AF379A0F4A4D CRC64;

Db 157 CNENYAGPNCERCAPGGYGNPLLI-----GSTCKRKCDCGNSDPNLIFEDC-DEVT 206 CC -! DISEASE: ANTIGEN IN THE AUTOIMMUNE DISEASE SJOEGREN'S SYNDROME AND CC IN HEPATITIS B.

Oy 167 KACK--YREATCSHCKSQVP---MIKLOKHEDTCPVVWS-CPHKCSVQTLRSELSA 219 CC -----

Db 207 GOCRLNRLNTGFCERCAPGGYGDARTAKN----CAVNGGGPD-----SYGE 254 CC -----

Oy 220 HLSECVNAPSTCFSKRYGCVF-----QGTNQKIAHEASSAVQVNLLKEW 265 CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires license agreement (See <http://www.isb-sib.ch/announce/>) or send an email to license@isb-sib.ch).

Db 255 CLEEFPEPPIGCD---KCWADTDLRLAALSIEEGSGVLSVSSGAHRAHVNEINAT 310 CC -----

Qy 266 SNSLEKKVSLQNE----SVEKNISIOSHNCFSFEIETEORKEMLNNE-----SK 314 DR EMBL; U41740; AAC50434.1; -

Db 311 YLLTKTSLSERENOYALRKIQINNANTMSLSDVEELVEKENQASRGKQLVQKESMT 370 DR EMBL; X82834; CAN58011.1; -

Oy 315 ILHQVQVID---SQAELKELDKIRPERQFWNE-----EADSMKSSVSLQNRV 360 DR EMBL; U31906; AAC51791.1; -

Db 491 Y-VRDAEDMRATAARQROHEKQEVRFQMEVNVNMLS 528 DR EMBL; X76942; CAN54261.1; -

DR Genew; HGNC:4427; Golgr4.

DR MM; 602509; -

DR InterPro; IPR000237; GRIP domain.

DR Pfam; PF01465; GRIP_1.

KW Golgi stack; Antigen; Coiled coil; Alternative splicing.

AC 013439; Q14436; Q12270; Q13654; PRT; 2230 AA.

AC 013439; Q14436; Q12270; Q13654; PRT; 2230 AA.

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Go1g1 autointeracting, golgin subfamily A 4 (Trans-golgi p230) (256 kDa golgin) (Golgin-245) (72.1 protein).

GN GOLG4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

RX MEDLINE=>96215236; PubMed=>8626529;

RA Erlich R., Gleeson P.A., Campbell P., Dietzsch E., Toh B.-H.; RT "Molecular characterization of trans-golgi p230: a human peripheral membrane protein encoded by a gene on chromosome 6p12-22 contains extensive coiled-coil alpha-helical domains and a granin motif.";

RL J. Biol. Chem. 271:8328-8337(1996).

RN [2]

RP SEQUENCE FROM N.A.

RA Seeling H.P.;

RL Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE OF 131-2230 FROM N.A.

RC TISSUE=Placenta;

RC MEDLINE=>96215112; PubMed=>8537393;

RA Fritsler M.J., Lung C.-C., Hamel J.C., Griffith K.J., Chan E.K.L.; RT "Molecular characterization of golgin-245, a novel Golgi complex protein containing a granin signature.";

RL J. Biol. Chem. 270:31262-31268(1995).

RN [4]

RP SEQUENCE OF 524-672 FROM N.A.

RC TISSUE=Gastric fundus;

RA Balague C.;

RL Thesis (1994). Instituto municipal de investigationes medicas, Spain.

-1 FUNCTION: MAY PLAY A ROLE IN VESTIGIAL TRANSPORT FROM THE TRANS-GOLGI.

CC -1 SUBCELLULAR LOCATION: ASSOCIATED WITH THE CYTOPLASMIC FACE OF THE GOLGI MEMBRANE.

CC -1 ALTERNATIVE PRODUCTS: At least 4 isoforms; 1 (shown here), 2, 3 and 4; are produced by alternative splicing.

Qy 13 LQPNPPKLQP-----RGAGSVLVPEOGGYKERFVKVVEDKYKCECRCLVLICNPQ 64 DR -----

Db 245 LKLPQLEPQAVFTKEENPESDGEPVY--EDGTSVKTLETLLQQRVKRQNLKRC--KE 300 DR -----

Qy 65 TCGHRHICESCHALLSSSSRSRKTACQESTIK----DKYFKDNCKRETLALOYCNE 119 DR -----

Db 301 TIQSHK--EQC--TLLSEK--EALQEQLDRLQLEKTRDLHMAETKLITOL--RD 350 DR -----

Qy 120 GRGCAEDITLGHLY-----HLRNNECQEELPQLRACKERKVLR-KOLDHVEKA-- 168 DR -----

Db 351 AKNLIEQLEODGMVIAETKROMHETLMKBEIAQLRSRKOMTQGEELREKSER 410 DR -----

Qy 169 CKYREATCSHCKSQVPMIKLOKHEDTCPVVWS-CPHKCSVQTLRSELSAHLSCVCNA 228 DR -----

Db 411 AAPEEL-----EKALSTAGKTEA-----RRKLAEMD----- 439 DR -----

Qy 229 STCSFKRYGCVFQGTNOQKIAHEASSAVQVNLLKEWNSLEKKVSLQNEVEKNS 288 DR -----

Db 440 ----- QKITEKTSSEERISLQQELSRSRQKEVVDVMKKSSEIQAKLQ 482 DR -----

Qy 289 SLH-NOICSFELI-----EROKMLRNNESKLHLQVQIDSQAE-KKELQ 334 DR -----

Db 483 KHEKEKELARKEDELTKLQLQTBERREFEQMKALEKQSEKQESLAEELLE, 542 DR -----

Qy 335 ETRP-FRQNWEBADSMKSSVSLQNRVTELESVDSQAGARNTGL---LESOLSRHD 388 DR -----

Db 543 OKKAIILSEENKLRLDQEAHYTRILEJESLSSLKSNQSKDLAGHLEAEKKN 602 DR -----

Qy 389 QTLSV---HOTRLADMRLRFQVLETAWSVNLWIRDYKRRKGAEVMGKTLISQPF 444 DR -----

Thu Dec 19 16:31:56 2002

us-08-813-323b-1.rsp

Page 14

Db 603 KEITVVMVEKHKTLESL-----
QY 445 YT 446
|
Db 639 QT 640

Search completed: December 19, 2002, 15:00:48
Job time : 19 secs